

GenCore version 5.1.3  
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OM protein - nucleotide search, using frame\_plus\_p2n model

Run on: January 16, 2003, 16:55:57 : Search time 110.214 seconds  
(without alignments)  
330.553 Million cell updates/sec

Title: US-09-856-070-18  
Perfect score: 24  
Sequence: 1 KEELM 5

Scoring table: BLOSUM62

Xgapop 10.0 ; Xgapext 0.5  
Ygapop 10.0 ; Ygapext 0.5  
Fgapop 6.0 ; Fgapext 7.0  
helop 6.0 ; helext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4105280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_plus\_p2n model -DEV=zip  
-Q=/cpu2\_1/USPT2\_spool/us09856070/runat\_14012004\_155834\_1621/app-query.fasta\_1\_1592  
-DB=GenEmbl1 -GEM1=fastap -SUFFIX=rge -MINMATCH=0.1 -PREFIX=0 -LOOPTXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LSP=45  
-DOCALIGN=200 -LHR\_SDOEXT=1 -LHR\_MAX=100 -LHR\_MIN=0 -AUPN=15 -MODE=LOCAL  
-OUTFMT=plc -NPM\_ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=20000000  
-USER=US09856070 -ASL=1 -CPU1=runat\_14012004\_155834\_1621 -NPM=F -LSP=4  
-WARN\_TIMEOUT=30 -THRPADS=1 -XGAPOP=10 -XGAPEXT=0 -WAIT -LNUHLW -DEV\_TIMEOUT=120  
-YGAPOP=10 -YGAPEXT=0 5 -DELCP=6 -DEFEXT=7

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hiq.\*
- 3: gb\_in.\*
- 4: gb\_cm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sv.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mus.\*
- 20: em\_ov.\*
- 21: em\_ov.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*

- 29: em\_vl.\*
- 30: em\_hiq\_hum.\*
- 31: em\_hiq\_inv.\*
- 32: em\_hiq\_other.\*
- 33: em\_hiq\_mus.\*
- 34: em\_hiq\_pln.\*
- 35: em\_hiq\_rnd.\*
- 36: em\_hiq\_mam.\*
- 37: em\_hiq\_vrt.\*
- 38: em\_sy.\*
- 39: em\_hiqo\_hum.\*
- 40: em\_hiqo\_mus.\*
- 41: em\_hiqo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	24	100.0	30	6	AX051524 Sequence
C 2	24	100.0	22	6	AX051145 Sequence
C 3	24	100.0	75	5	AF033542 Coratyps
C 4	24	100.0	77	6	A25925 MGXXX promo
C 5	24	100.0	77	6	A25926 MGXXX promo
C 6	24	100.0	128	9	HS195C10T
C 7	24	100.0	129	9	H9195C10H
C 8	24	100.0	162	9	HSLAS80B
C 9	24	100.0	195	9	HSU55185
C 10	24	100.0	226	11	GL16198
C 11	24	100.0	242	9	HSAL11611
C 12	24	100.0	348	3	AF082538
C 13	24	100.0	348	11	A0928715
C 14	24	100.0	351	11	HSP1802
C 15	24	100.0	352	11	G25533
C 16	24	100.0	352	11	G55356
C 17	24	100.0	362	6	AX337439
C 18	24	100.0	371	11	HSB3082E9
C 19	24	100.0	372	3	AF152580
C 20	24	100.0	377	3	AF336818
C 21	24	100.0	384	11	G17562
C 22	24	100.0	396	6	AX071771
C 23	24	100.0	399	6	AX071365
C 24	24	100.0	410	3	AF390903
C 25	24	100.0	426	5	AF306569
C 26	24	100.0	431	9	HUMSP25
C 27	24	100.0	438	11	G28129
C 28	24	100.0	453	6	AX392765
C 29	24	100.0	460	9	AF190059
C 30	24	100.0	471	9	AF188896
C 31	24	100.0	472	3	AF095204
C 32	24	100.0	475	9	AF188897
C 33	24	100.0	478	9	AF189213
C 34	24	100.0	489	9	AF187552
C 35	24	100.0	507	14	VVLLENV
C 36	24	100.0	508	8	AF482638
C 37	24	100.0	523	11	G20947
C 38	24	100.0	539	6	AX106210
C 39	24	100.0	539	6	AX106529
C 40	24	100.0	539	6	AX140820
C 41	24	100.0	539	6	AX205680
C 42	24	100.0	539	6	AX267336
C 43	24	100.0	542	6	AX046513
C 44	24	100.0	544	11	G58413
C 45	24	100.0	545	6	AX387845

ALIGNMENTS

RESULT 1

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AR162524/c
LOCUS AR162524 20 bp DNA linear PAT 17 OCT 2001
DEFINITION Sequence 28 from patent US 6258601.
ACCESSION AR162524
VERSION AR162524.1 GI:16225747
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mania,B.P. and Cowser,L.M.
TITLE Antisense modulation of ubiquitin protein ligase expression
JOURNAL Patent: US 6258601 A 28 10 2001 2001
FEATURES
location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 4 a 8 c 0 g 8 t
ORIGIN
1
|||||
20

Alignment Scores:
Pred. No.: 28 q Length: 20
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:

US-09-856-070-18 (1-5) x AR162524 (1-20)

QY 1 LysGluGluLeuMet 5
DB 17 AAAGAAGAGTTGATG 4

RESULT 2
LOCUS AX053145/c 22 bp DNA linear PAT 13 JAN 2001
DEFINITION Sequence 7 from Patent WO0073329
ACCESSION AX053145
VERSION AX053145.1 GI:12227508
KEYWORDS
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 22)
AUTHORS Baron,M
TITLE Uses of notch-related genes
JOURNAL Patent: WO 0073329-A 7 07-DEC-2000;
THE VICTORIA UNIVERSITY OF MANCHESTER (GB)
FEATURES
location/Qualifiers
1..22
/organism="Drosophila sp."
/db_xref="taxon:7242"
BASE COUNT 4 a 9 c 1 g 8 t
ORIGIN
1
|||||
22

Alignment Scores:
Pred. No.: 31.5 Length: 22
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:

US-09-856-070-18 (1-5) x AX053145 (1-22)

QY 1 LysGluGluLeuMet 5
DB 19 AAAGAAGAGTTGATG 5

RESULT 3
LOCUS AF033542/c 75 bp DNA linear PAT 06 MAR 1995
DEFINITION Coragyps atratus P302 microsatellite sequence.
ACCESSION AF033542
VERSION AF033542.1 GI:12642042
KEYWORDS
SOURCE Coragyps atratus.
ORGANISM Coragyps atratus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neoquathae; Ciconiiformes; Cathartidae;
Coragyps.
REFERENCE 1 (bases 1 to 75)
AUTHORS Primer,C.R., and Ellegren,H.
TITLE A wide-range survey of cross-species microsatellite amplification
in birds
JOURNAL Mol. Ecol. 5 (3), 365-378 (1996)
MEDLINE 95266697
PUBMED 8684957
REFERENCE 2 (bases 1 to 75)
AUTHORS Primer,C.R., and Ellegren,H.
TITLE Patterns of molecular evolution in avian microsatellites
JOURNAL Mol. Biol. Evol. 15 (8), 997-1008 (1998)
MEDLINE 98384839
PUBMED 9718727
REFERENCE 3 (bases 1 to 75)
AUTHORS Primer,C.R., and Ellegren,H.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1997) Animal Breeding and Genetics, Biomedical
Centre, Swedish University of Agricultural Sciences, Box 597,
Uppsala S-75124, Sweden
FEATURES
location/Qualifiers
1..75
/organism="Coragyps atratus"
/db_xref="taxon:33614"
repeat_region
12..19
/note="a homolog of the pied flycatcher microsatellite
sequence, GenBank Accession Number X84361"
/ft_family="P302 microsatellite"
/ft_type=tandem
/ft_unit=ct
BASE COUNT 13 a 24 c 12 g 26 t
ORIGIN
1
|||||
75

Alignment Scores:
Pred. No.: 97.2 Length: 75
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:

US-09-856-070-18 (1-5) x AF033542 (1-75)

QY 1 LysGluGluLeuMet 5
DB 63 AAGGAGAAITGATG 49

RESULT 4
LOCUS A25925/c 77 bp DNA linear PAT 06 MAR 1995
DEFINITION M2XXX promoter sequences.
ACCESSION A25925
VERSION A25925.1 GI:833591
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
FEATURES
location/Qualifiers
1..77
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 19 a 13 c 9 g 36 t
ORIGIN
1
|||||
77

```

```

Alignment Scores:
Pred. No.: 99.6 Length: 77
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-18 (1-5) x A25926 (1-77)
QY 1 LysGluGluLeuMet 5
DB 23 AACGACGAATTAAG 5

RESULT 5
LOCUS A25926 77 bp DNA linear PAT 06-MAR-1995
DEFINITION MXXX promoter sequences.
ACCESSION A25926
VERSION A25926.1 GI:833683
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
    source
        location/Qualifiers
            1..77
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                13 q 19 t

BASE COUNT 36 a 9 c 13 g
ORIGIN
Alignment Scores:
Pred. No.: 99.6 Length: 77
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-18 (1-5) x A25926 (1-77)
QY 1 LysGluGluLeuMet 5
DB 59 AACGACGAATTAAG 73

RESULT 6
LOCUS HS195C10F/C 128 bp DNA linear PPI 19-OCT-1995
DEFINITION H.sapiens CpG island DNA genomic MseI fragment, clone 195c10, forward read cpg195c10.ft1a.
ACCESSION 260206
VERSION 260206.1 GI:1032110
KEYWORDS CpG island; genomic MseI fragment.
SOURCE CpG island; genomic MseI fragment.
ORGANISM Homo sapiens
    location/Qualifiers
        1..128
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="195c10"
            /sex="male"
            /tissue_type="blood"
            /clone_lib="CGI-1"
            /dev_stage="adult"
            23 q 39 t 3 others

REFERENCE
AUTHORS Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column
JOURNAL Nat. Genet. 6 (3), 236-244 (1994)
MEDLINE 94282070
PUBMED 8012384
COMMENT Vector: pCEM-52f(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1PQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: bihelp@hgmp.mrc.ac.uk.

FEATURES
    source
        location/Qualifiers
            1..129
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="195c10"
                /sex="male"
                /tissue_type="blood"
                /clone_lib="CGI-1"
                /dev_stage="adult"
                23 q 39 t 3 others

BASE COUNT 54 a 10 c 23 g
ORIGIN
Alignment Scores:
Pred. No.: 160 Length: 129
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-856-070-18 (1-5) x HS195C10F (1-128)
QY 1 LysGluGluLeuMet 5
DB 76 AAGGACGAATTAAG 62

RESULT 7
LOCUS HS195C10R 129 bp DNA linear PRI 19-OCT-1995
DEFINITION H.sapiens CpG island DNA genomic MseI fragment, clone 195c10, reverse read cpg195c10.ft1a.
ACCESSION 260207
VERSION 260207.1 GI:1032110
KEYWORDS CpG island; genomic MseI fragment.
SOURCE CpG island; genomic MseI fragment.
ORGANISM Homo sapiens
    location/Qualifiers
        1..129
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="195c10"
            /sex="male"
            /tissue_type="blood"
            /clone_lib="CGI-1"
            /dev_stage="adult"
            23 q 39 t 3 others

REFERENCE
AUTHORS Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column
JOURNAL Nat. Genet. 6 (3), 236-244 (1994)
MEDLINE 94282070
PUBMED 8012384
COMMENT Vector: pCEM-52f(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1PQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: bihelp@hgmp.mrc.ac.uk.

FEATURES
    source
        location/Qualifiers
            1..129
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="195c10"
                /sex="male"
                /tissue_type="blood"
                /clone_lib="CGI-1"
                /dev_stage="adult"
                23 q 39 t 3 others

BASE COUNT 54 a 10 c 23 g
ORIGIN
Alignment Scores:
Pred. No.: 160 Length: 129
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

```

US 09 856-070 18 (1-5) x HS195610R (1-129)

QY 1 LysGluGluLeuMet 5  
 DB 55 AAGAGAGAGTTCATG 69

# RESULT 8

HS1AS80B 162 bp DNA linear PRI 22-AUG 1996  
 DEFINITION H.sapiens DNA for loop attachment sequence (clone LAS80B).

ACCESSION X91577

VERSION X91577.1 GI:987936

KEYWORDS loop attachment sequence.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 162)

AUTHORS Cook, P.R.

TITLE Direct Submission

JOURNAL Submitted (14-SEP-1995) P.R. Cook, Sir William Dunn School of

Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE,

UK

REFERENCE 2 (bases 1 to 162)

AUTHORS Jackson, D.A., Bartlett, J., and Cook, P.R.

TITLE Sequences attaching loops of nuclear and mitochondrial DNA to

underlying structures in human cells: the role of transcription

units

JOURNAL Nucleic Acids Res. 24 (7), 1212-1219 (1996)

MEDLINE 9418852

PMID 8614621

## FEATURES

source

1..162 Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="LAS80B"

/cell\_line="HeLa"

/clone\_lib="DNA loop attachment sequences (LAS)"

misc\_feature 1..162

/note="DNA loop attachment site (LAS)"

BASE COUNT 54 a 34 c 27 q 47 t

## Alignment Scores:

Pred. No.: 197 Length: 162

Score: 24.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US 09 856-070 18 (1-5) x HS1AS80B (1-162)

QY 1 LysGluGluLeuMet 5

DB 144 AAGAGAGTTCATG 158

# RESULT 9

HS055185

LOCUS

DEFINITION Human oral cancer candidate gene mRNA, clone T9, 3' end.

ACCESSION U55185

VERSION U55185.1 GI:1314791

KEYWORDS

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 195)

AUTHORS Wong, D.T.W., and Kao, S.Y.

TITLE Direct Submission

JOURNAL Submitted (15-APR-1996) D.T.W. Wong, Oral Pathology, Harvard School

of Dental Medicine, 188 Longwood Avenue, Boston, MA 02115, USA

## FEATURES

source

1..195 Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="T9"

/cell\_line="oral cancer cell lines SC015, SC025, R0"

/note="induced by retinoic acid; isolated with primer

combination 19"

BASE COUNT 83 a 33 c 29 g 50 t

## ORIGIN

Alignment Scores:

Pred. No.: 234 Length: 195

Score: 24.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-856-070-18 (1-5) x HS055185 (1-195)

QY 1 LysGluGluLeuMet 5

DB 48 AAGAGAGTTCATG 62

RESULT 10

GL6198

LOCUS

GL6198

DEFINITION Human STS 963FVL clone 963F9, sequence tagged site.

ACCESSION GL6198

VERSION GL6198.1 GI:1592373

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens vector-pYAC4 host-S. cerevisiae.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 226)

AUTHORS Thompson, D.H. and Hodgardus, C.

TITLE Structure and physical mapping of the human leptin receptor gene

(OBR): located at the acute insulin secretion locus

Unpublished (1996)

JOURNAL

COMMENT

Contact: D. Bruce Thompson

Clinical Diabetes and Nutrition Section

National Institute of Diabetes and Digestive and Kidney Diseases

4212 N. 16th Street, Phoenix, AZ 85016.

Tel: 602-263-1556

Fax: 602-263-1647

Email: dhj@ku.nih.gov

Primer A: TTAAAGAGAGTAAAGCCAAAC

Primer B: CACAGTTCGTGTTGTTGTTGTTG

STS size: 171

PCR profile:

94°C 3 minutes, 94°C 30 seconds, 51°C 60 seconds, 72°C 45 seconds

25 cycles.

## FEATURES

source

1..226 Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

STS 10..180

primer\_bind 10..114

primer\_bind complement(157..180)

BASE COUNT 94 a 53 c 36 g 43 t

## ORIGIN

Alignment Scores:

Pred. No.: 268 Length: 226

Score: 24.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

```

Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-856-070-18 (1-5) x G16198 (1-226)

QY 1 LysGluGluLeuMet 5
|||||
DB 13 AAAGAAGAACTAATG 27

RESULT 11
HSA131611/c
LOCUS Homo sapiens egl gene promoter and 5'UTR. 242 bp DNA linear PRI 18-MAY-2002
DEFINITION AJ131611
ACCESSION AJ131611.1 GI:7478722
VERSION egl gene, epidermal growth factor.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Shalhoub, M., Pravica, V., Nasreen, N., Fakhoury, H., Fryer, A.A.,
Strange, R.C., Hutchinson, P.E., Osborne, J.E., Lear, T.T., Smith, A.C.
and Hutchinson, I.V.
TITLE Association between functional polymorphism in EGF gene and
malignant melanoma
JOURNAL Lancet 359 (9304), 397-401 (2002)
MEDLINE 21833709
PUBMED 11845111
REFERENCE 2 (bases 1 to 242)
AUTHORS Fakhoury, H.
TITLE Direct Submission
JOURNAL Submitted (22 DEC-1998) Fakhoury H., Immunology Research Group,
University of Manchester, Stepford Building, Oxford Road,
Manchester M13 9PT, UNITED KINGDOM
FEATURES
Source 1..242
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..242
/promoter /gene="egf"
5'UTP <1..78
/standard_name="epidermal growth factor"
/variation 79..212
/standard_name="epidermal growth factor"
139
/gene="egf"
BASE COUNT 64 a 54 c 52 g 72 t
ORIGIN
Alignment Scores:
Pred. No.: 285 Length: 242
Score: 24.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-856-070-18 (1-5) x HSA131611 (1-242)
QY 1 LysGluGluLeuMet 5
|||||
DB 166 AAAGAAGAACTAATG 152

RESULT 12
AF082518
LOCUS Entamoeba invadens ADP-ribosylation factor (ARF) gene, partial cds. 338 bp DNA linear INV 25-MAY-1999
DEFINITION AF082518
ACCESSION AF082518.1 GI:3746800
VERSION

Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-856-070-18 (1-5) x AF082518 (1-338)
QY 1 LysGluGluLeuMet 5
|||||
DB 256 AAAGAAGAACTAATG 270

RESULT 13
AF082715
LOCUS Rattus norvegicus, GTSUKA clone, G16.15/01402, microsatellite
DEFINITION AF082715
ACCESSION AF082715.1 GI:4518638
VERSION STS.
KEYWORDS Rattus norvegicus LNA, clone:016.15/01402.
SOURCE Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Watanabe, T.K., Hishigaki, H., Kanemoto, N., Miyakita-Mizoguchi, A.,
Oga, K., Okuno, S., Ono, F., Tsuji, A., Hayashi, H., Adachi, M.,
Yamasaki, Y., Iriye, Y., Takahashi, E., Takagi, T., Nakamura, Y. and
Tanigami, A.
TITLE The large-scale mapping of rat microsatellite markers
JOURNAL Unpublished

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## KEYWORDS

SOURCE

## ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-856-070-18 (1-5) x AF082518 (1-338)

QY

DB

RESULT 13

AF082715

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

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Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-09-856-070-18 (1-5) x G25533 (1-352)

QY 1 LysGluGluLeuMet 5

DB 134 AAGGAAGAGCTCATG 148

Search completed: January 16, 2003, 19:02:40  
 Job time : 442.214 secs

